

## SEQUENCE LISTING

<110> REGENTS OF THE UNIVERSITY OF CALIFORNIA  
 TSIEN, Roger  
 Campbell, Robert

<120> NON-OLIGOMERIZING FLUORESCENT PROTEINS

<130> REGEN1530-2

<140> Herewith

<141> 2001-05-24

<160> 29

<170> PatentIn version 3.0

<210> 1

<211> 716

<212> DNA

<213> Aequorea victoria

<220>

<221> CDS

<222> (1)..(714)

<400> 1

|   |    |
|---|----|
| atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att ctt gtt | 48 |
| Met Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val     |    |
| 1 5 10 15   |    |

|   |    |
|---|----|
| gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag | 96 |
| Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu |    |
| 20 25 30  |    |

|   |     |
|---|-----|
| ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc | 144 |
| Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys |     |
| 35 40 45  |     |

|   |     |
|---|-----|
| act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc | 192 |
| Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe |     |
| 50 55 60  |     |

|   |     |
|---|-----|
| tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg aaa cag | 240 |
| Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln |     |
| 65 70 75 80   |     |

|   |     |
|---|-----|
| cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga | 288 |
| His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg |     |
| 85 90 95  |     |

|   |     |
|---|-----|
| act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc | 336 |
| Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val |     |
| 100 105 110   |     |

|   |     |
|---|-----|
| aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att | 384 |
| Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile |     |
| 115 120 125   |     |

|   |     |
|---|-----|
| gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac | 432 |
| Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn |     |

| 130   | 135 | 140 |     |
|---|-----|-----|-----|
| tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat gga |     |     | 480 |
| Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly |     |     |     |
| 145   | 150 | 155 | 160 |
| atc aaa gtt aac ttc aaa att aga cac aac att gaa gat gga agc gtt |     |     | 528 |
| Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val |     |     |     |
|   | 165 | 170 | 175 |
| caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct |     |     | 576 |
| Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro |     |     |     |
|   | 180 | 185 | 190 |
| gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcg |     |     | 624 |
| Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser |     |     |     |
|   | 195 | 200 | 205 |
| aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta |     |     | 672 |
| Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val |     |     |     |
|   | 210 | 215 | 220 |
| aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa ta      |     |     | 716 |
| Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys         |     |     |     |
| 225   | 230 | 235 |     |

<210> 2  
 <211> 238  
 <212> PRT  
 <213> Aequorea victoria

<400> 2

|   |     |     |     |
|---|-----|-----|-----|
| Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val |     |     |     |
| 1   | 5   | 10  | 15  |
| Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu |     |     |     |
|   | 20  | 25  | 30  |
| Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys |     |     |     |
|   | 35  | 40  | 45  |
| Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe |     |     |     |
|   | 50  | 55  | 60  |
| Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln |     |     |     |
| 65  | 70  | 75  | 80  |
| His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg |     |     |     |
|   | 85  | 90  | 95  |
| Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val |     |     |     |
|   | 100 | 105 | 110 |

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

<210> 3  
 <211> 720  
 <212> DNA  
 <213> Aequorea victoria

<220>  
 <221> CDS  
 <222> (1)..(720)

<400> 3  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

| 65  | 70  | 75  | 80  |     |
|---|-----|-----|-----|-----|
| cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag |     |     |     | 288 |
| Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu | 85  | 90  | 95  |     |
| cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag |     |     |     | 336 |
| Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu | 100 | 105 | 110 |     |
| gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc |     |     |     | 384 |
| Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly | 115 | 120 | 125 |     |
| atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac |     |     |     | 432 |
| Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr | 130 | 135 | 140 |     |
| aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac |     |     |     | 480 |
| Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn | 145 | 150 | 155 | 160 |
| ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc |     |     |     | 528 |
| Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser | 165 | 170 | 175 |     |
| gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc |     |     |     | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly | 180 | 185 | 190 |     |
| ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg |     |     |     | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu | 195 | 200 | 205 |     |
| agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc |     |     |     | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe | 210 | 215 | 220 |     |
| gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa |     |     |     | 720 |
| Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys     | 225 | 230 | 235 |     |

&lt;210&gt; 4

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Aequorea victoria

&lt;400&gt; 4

|   |   |    |    |
|---|---|----|----|
| Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu |   |    |    |
| 1   | 5 | 10 | 15 |

|   |    |    |  |
|---|----|----|--|
| Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly |    |    |  |
| 20  | 25 | 30 |  |

|   |    |    |  |
|---|----|----|--|
| Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile |    |    |  |
| 35  | 40 | 45 |  |

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
225 230 235

<210> 5  
<211> 720  
<212> DNA  
<213> Aequorea victoria

<220>  
<221> CDS  
<222> (1)..(720)

<400> 5  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

| 1   | 5 | 10  | 15  |     |
|---|---|-----|-----|-----|
| gtc gag ctg gac ggc gac gta aac ggc cac agg ttc agc gtg tcc ggc |   |     |     | 96  |
| Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly |   |     |     |     |
| 20  |   | 25  | 30  |     |
| gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc |   |     |     | 144 |
| Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile |   |     |     |     |
| 35  |   | 40  | 45  |     |
| tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc |   |     |     | 192 |
| Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr |   |     |     |     |
| 50  |   | 55  | 60  |     |
| ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag |   |     |     | 240 |
| Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys |   |     |     |     |
| 65  |   | 70  | 75  | 80  |
| cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag |   |     |     | 288 |
| Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu |   |     |     |     |
| 85  |   | 90  | 95  |     |
| cgt acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag |   |     |     | 336 |
| Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu |   |     |     |     |
| 100   |   | 105 | 110 |     |
| gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc |   |     |     | 384 |
| Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly |   |     |     |     |
| 115   |   | 120 | 125 |     |
| atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac |   |     |     | 432 |
| Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr |   |     |     |     |
| 130   |   | 135 | 140 |     |
| aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac |   |     |     | 480 |
| Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn |   |     |     |     |
| 145   |   | 150 | 155 | 160 |
| ggc atc aag gcc cac ttc aag atc cgc cac aac atc gag gac ggc agc |   |     |     | 528 |
| Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser |   |     |     |     |
| 165   |   | 170 | 175 |     |
| gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc |   |     |     | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly |   |     |     |     |
| 180   |   | 185 | 190 |     |
| ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg |   |     |     | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu |   |     |     |     |
| 195   |   | 200 | 205 |     |
| agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc |   |     |     | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe |   |     |     |     |
| 210   |   | 215 | 220 |     |
| gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa |   |     |     | 720 |
| Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys     |   |     |     |     |
| 225   |   | 230 | 235 |     |

&lt;210&gt; 6

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Aequorea victoria

&lt;400&gt; 6

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn  
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

<210> 7  
 <211> 720  
 <212> DNA  
 <213> *Aequorea victoria*

<220>  
 <221> CDS  
 <222> (1) .. (720)

<400> 7  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ttc ggc tac ggc gtg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190



agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672  
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa 720  
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
225 230 235

```
<210> 8
<211> 239
<212> PRT
<213> Aequorea victoria
```

<400> 8

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu  
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

<210> 9  
 <211> 720  
 <212> DNA  
 <213> Aequorea victoria

<220>  
 <221> CDS  
 <222> (1)..(720)

<400> 9  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg 624  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu  
 195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672  
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa 720  
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

<210> 10

<211> 239

<212> PRT

<213> Aequorea victoria

<400> 10

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu  
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
225 230 235

<210> 11  
<211> 859  
<212> DNA  
<213> Discosoma sp.

<220>  
<221> CDS  
<222> (54)..(731)

<400> 11  
gtttcagcca gtgacgggtca gtgacagggt gagccacttg gtataccaac aaa atg 56  
Met  
1

agg tct tcc aag aat gtt atc aag gag ttc atg agg ttt aag gtt cgc 104  
Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg  
5 10 15

atg gaa gga acg gtc aat ggg cac gag ttt gaa ata gaa ggc gaa gga 152  
Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly  
20 25 30

gag ggg agg cca tac gaa ggc cac aat acc gta aag ctt aag gta acc 200  
Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val Thr  
35 40 45

aag ggg gga cct ttg cca ttt gct tgg gat att ttg tca cca caa ttt 248  
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe  
50 55 60 65  
cag tat gga agc aag gta tat gtc aag cac cct gcc gac ata cca gac 296  
Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro Asp  
70 75 80  
tat aaa aag ctg tca ttt cct gaa gga ttt aaa tgg gaa agg gtc atg 344  
Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met  
85 90 95  
aac ttt gaa gac ggt ggc gtc gtt act gta acc cag gat tcc agt ttg 392  
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu  
100 105 110  
cag gat ggc tgt ttc atc tac aag gtc aag ttc att ggc gtg aac ttt 440  
Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn Phe  
115 120 125  
cct tcc gat gga cct gtt atg caa aag aag aca atg ggc tgg gaa gcc 488  
Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala  
130 135 140 145  
agc act gag cgt ttg tat cct cgt gat ggc gtg ttg aaa gga gag att 536  
Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu Ile  
150 155 160  
cat aag gct ctg aag ctg aaa gac ggt ggt cat tac cta gtt gaa ttc 584  
His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu Phe  
165 170 175  
aaa agt att tac atg gca aag aag cct gtg cag cta cca ggg tac tac 632  
Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr Tyr  
180 185 190  
tat gtt gac tcc aaa ctg gat ata aca agc cac aac gaa gac tat aca 680  
Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr  
195 200 205  
atc gtt gag cag tat gaa aga acc gag gga cgc cac cat ctg ttc ctt 728  
Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe Leu  
210 215 220 225  
taa ggctgaactt ggctcagacg tgggtgagcg gtaatgacca caaaaggcag 781  
cgaagaaaaa ccatgatcgt tttttttagg ttggcagcct gaaatcgtag gaaatacatc 841  
agaaatgtta caaacagg 859

<210> 12  
<211> 225  
<212> PRT  
<213> Discosoma sp.

<400> 12

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val  
1 5 10 15

Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu  
20 25 30

Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val  
35 40 45

Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln  
50 55 60

Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro  
65 70 75 80

Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val  
85 90 95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser  
100 105 110

Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn  
115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu  
130 135 140

Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu  
145 150 155 160

Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu  
165 170 175

Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr  
180 185 190

Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr  
195 200 205

Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe  
210 215 220

Leu  
225

<210> 13  
<211> 42  
<212> DNA

<213> Artificial

<220>

<223> PRIMER A206K top

<400> 13

cagtccaagc tgagcaaaga ccccaacgag aagcgcgatc ac

42

<210> 14

<211> 42

<212> DNA

<213> Artificial

<220>

<223> PRIMER A206K bottom

<400> 14

gtgatcgcg ttctcgttgg ggtctttgct cagcttggac tg

42

<210> 15

<211> 36

<212> DNA

<213> Artificial

<220>

<223> PRIMER L221K top

<400> 15

cacatggtcc tgaaggagtt cgtgaccgcc gccggg

36

<210> 16

<211> 36

<212> DNA

<213> Artificial

<220>

<223> PRIMER L221K bottom

<400> 16

cccggcggcg gtcacgaact ccttcaggac catgtg

36

<210> 17

<211> 36

<212> DNA

<213> Artificial

<220>

<223> PRIMER F223R top

<400> 17

cacatggtcc tgctggagcg cgtgaccgcc gccggg

36

<210> 18

<211> 36

<212> DNA

<213> Artificial

<220>  
 <223> PRIMER F223R bottom

<400> 18  
 cccggcgggcg gtcacgcgct ccagcaggac catgtg 36

<210> 19  
 <211> 36  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PRIMER L221K/F223R top

<400> 19  
 cacatcgtcc tgaaggagcg cgtgaccgcc gccggg 36

<210> 20  
 <211> 36  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PRIMER L221K/F223R bottom

<400> 20  
 cccggcgggcg gtcacgcgct ccttcaggac catgtg 36

<210> 21  
 <211> 33  
 <212> PRT  
 <213> Artificial

<220>  
 <223> ADDITIONAL 33 AMINO ACIDS TAG TO THE N-TERMINUS OF THE GFPS

<400> 21

Met Arg Gly Ser His His His His His Gly Met Ala Ser Met Thr  
 1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp  
 20 25 30

Pro

<210> 22  
 <211> 33  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PRIMER I125K

<400> 22  
 tacaaggtga agttcaaggc cgtgaacttc ccc 33



<210> 23  
 <211> 33  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PRIMER L125K reverse

<400> 23  
 ggggaagttc acgcccttga acttcacctt gta 33

<210> 24  
 <211> 33  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PRIMER I125R forward

<400> 24  
 tacaaggtga agttccgagg cgtgaacttc ccc 33

<210> 25  
 <211> 33  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PRIMER I125R reverse

<400> 25  
 ggggaagttc acgccgaggga acttcacctt gta 33

<210> 26  
 <211> 18  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic peptide

<400> 26

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr  
 1 5 10 15

Lys Gly

<210> 27  
 <211> 86  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Primer for PCR

<400> 27  
ccggatcccc ttggtgctg cctctccgc tgccaggctt gccgtgccg ctggtgctgc 60  
caaggaacag atggtggcgt cctcgc 86

<210> 28  
<211> 86  
<212> DNA  
<213> Artificial

<220>  
<223> Primer for PCR

<400> 28  
ccggatcccc cttggtgctg cctccccgc tgccgggctt cccgtcccg ctggtgctgc 60  
ccaggaacag gtggtggcgg cctcgc 86

<210> 29  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> Primer for PCR

<400> 29  
gtacgacgat gacgataagg atcc 24